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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Soll, Dieter
- (ii) TITLE OF INVENTION: GLU-TRAN AMIDOTRANSFERASE - A NOVEL
ESSENTIAL TRANSLATIONAL COMPONENT
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 - (B) STREET: 1800 M Street, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20036-5869
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US Unassigned
 - (B) FILING DATE: 03-FEB-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/037,275
 - (B) FILING DATE: 03-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Adler, Reid G.
 - (B) REGISTRATION NUMBER: 30,988
 - (C) REFERENCE/DOCKET NUMBER: 044574-5024-WO
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-467-7000
 - (B) TELEFAX: 202-467-7176

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: join(1..54, 58..390, 394..1866, 1870..3303, 3310
..3321, 3325..3348, 3352..3429, 3433..3471, 3475
..3480, 3484..3495)

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.xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAA TTC GAT CCT GTC TCA AGG DGT TTT GTT GCT TTA AAG GGC TTG TTT	45
Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe	
1 5 10 15	
TTG ATA TGA TCA GTA TTA TAT GAC TTA ACG GAG AAA TAT GTG GAG GTG	96
Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val	
20 25 30	
GAT CAT ATG TCA CGA ATT TCA ATA GAA GAA GTA AAG CAC GTT GCG CAC	144
Asp His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His	
35 40 45	
CTT GCA AGA CTT GCG ATT ACT GAA GAA GAA GCA AAA ATG TTC ACT GAA	192
Leu Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu	
50 55 60	
CAG CTC GAC AGT ATC ATT TCA TTT GCC GAG GAG CTT AAT GAG GTT AAC	240
Gln Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn	
65 70 75	
ACA GAC AAT GTG GAG CCT ACA ACT CAC GTG CTG AAA ATG AAA AAT GTC	288
Thr Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val	
80 85 90 95	
ATG AGA GAA GAT GAA GCG GGT AAA GGT CTT CCG GTT GAG GAT GTC ATG	336
Met Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met	
100 105 110	
AAA AAT GCG CCT GAC CAT AAA GAC GGC TAT ATT CGT GTG CCA TCA ATT	384
Lys Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile	
115 120 125	
CTG GAC TAA AGG AGG GAC ACA AGA ATG TCA TTA TTT GAT CAT AAA ATC	432
Leu Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile	
130 135 140	
ACA GAA TTA AAA CAG CTC ATA CAT AAA AAA GAG ATT AAG ATT TCT GAT	480
Thr Glu Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp	
145 150 155	
CTG GTT GAT GAA TCT TAT AAA CGC ATC CAA GCG GTT GAT GAT AAG GTA	528
Leu Val Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val	
160 165 170	
CAA GCC TTT TTG GCA TTA GAT GAA GAA AGA GCG CGC GCA TAC GCG AAG	576
Gln Ala Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys	
175 180 185 190	
GAG CTT GAT GAG GCG GTT GAC GGC CGT TCT GAG CAC GGT CTT CTT TTC	624
Glu Leu Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe	
195 200 205	
GGT ATG CCG ATC GGC GTA AAA GAT AAT ATC GTA ACA AAA GGG CTG CGC	672
Gly Met Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg	
210 215 220	

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ACA ACA TGC TCC AGC AAA ATT CTC GAA AAC TTT GAT CCG ATT TAC GAT Thr Thr Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp 225 230 235	700
GCT ACT GTC GTT CAG CGC CTT CAA GAC GCT GAA GCG CTC ACA ATC GGA Ala Thr Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly 240 245 250	768
AAA CTG AAC ATG GAC GAA TTC GCC ATG GGG TCA TCT ACA GAA AAC TCA Lys Leu Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser 255 260 265 270	816
GCT TAC AAG CTG ACG AAA AAC CCT TGG AAC CTG GAT ACA GTT CCC GGC Ala Tyr Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly 275 280 285	864
GGT TCA AGC GGC GGA TCT GCA GCT GCG GTT GCT GCG GGA GAA GTT CCG Gly Ser Ser Gly Gly Ser Ala Ala Val Ala Ala Gly Glu Val Pro 290 295 300	912
TTT TCT CTT GGA TCT GAC ACA GGC GGC TCC ATC CGT CAG CCG GCA TCT Phe Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser 305 310 315	960
TTC TGC GGC GTT GTC GGA TTA AAA CCT ACA TAC GGA CGT GTA TCT CGT Phe Cys Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg 320 325 330	1008
TAC GGC CTG GTC GCA TTT GCG TCT TCA TTG GAC CAA ATC GGA CCG ATT Tyr Gly Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile 335 340 345 350	1056
ACA CGT ACG GTT GAG GAT AAC GCG TTT TTA CTT CAA GCG ATT TCC GGC Thr Arg Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly 355 360 365	1104
GTA GAC AAA ATG GAC TCT ACG AGT GCA AAT GTG GAC GTG CCT GAT TTT Val Asp Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe 370 375 380	1152
CTT TCT TCA TTA ACT GGC GAC ATC AAA GGA CTG AAA ATC GCC GTT CCG Leu Ser Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro 385 390 395	1200
AAA GAA TAC CTT GGT GAA GGT GTC GGC AAA GAA GCG AGA GAA TCT GTC Lys Glu Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val 400 405 410	1248
TTG GCA GCG CTG AAA GTC CTT GAA GGT CTC GGC GCT ACA TGG GAA GAA Leu Ala Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu 415 420 425 430	1296
GTG TCT CTT CCG CAC AGT AAA TAC GCG CTT GCG ACA TAT TAC CTG CTG Val Ser Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu 435 440 445	1344
TCA TCT TCT GAA GCG TCA GCG AAC CTT GCA GCG TTT GAC GGC ATC CCG Ser Ser Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg 450 455 460	1392

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TAC GGC TAC CGC ACA GAC AAC GCG GAT AAC CTG ATC GAC CTT TAC AAG Tyr Gly Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys 465 470 475	1441
CAA ACG CGC GCT GAA GGT TTC GGA AAT GAA GTC AAA CCG CGC ATC ATG Gln Thr Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met 480 485 490	1489
CTC GGA ACG TTT GCT TTA AGC TCA GGC TAC TAC GAT CCG TAC TAC AAA Leu Gly Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys 495 500 505 510	1536
AAA GCG CAA AAA GTG CGT ACG TTG ATT AAG AAG GAT TTC GAG GAC GTA Lys Ala Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val 515 520 525	1584
TTT GAA AAA TAT GAT GTT ATT GTT GGA CCG ACT ACA CCG ACA CCT GCG Phe Glu Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala 530 535 540	1632
TTT AAA ATC GGT GAA AAC ACG AAG GAT CCG CTC ACA ATG TAC GCA AAC Phe Lys Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn 545 550 555	1680
GAT ATC TTA ACG ATT CCG GTC AAC CTT GCG GCG TAC CCG GAA TCA GGT Asp Ile Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly 560 565 570	1728
GCC ATG CCG TTA GCA GAC GGA CTT CCG CTC GGC CTG CAA ATC ATC GGA Ala Met Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly 575 580 585 590	1776
AAA CAC TTT GAT GAA GCA CTG TAT ACC GCG TTG CTC ATG CAT TTG AAC Lys His Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn 595 600 605	1824
AAG CAA CAG ACC ATC ATA AAG CAA AAC CTG AAC TGT AAG GGG Lys Gln Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly 610 615 620	1866
TGA AAA GAA TTG AAC TTT GAA ACG GTA ATC GGA CTT GAA GTC CAC GTT Lys Glu Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val 625 630 635	1914
GAG TTA AAA ACA AAA TCA AAA ATT TTC TCA AGC TCT CCA ACG CCA TTC Glu Leu Lys Thr Lys Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe 640 645 650	1962
GGC GCG GAG GCG AAT ACG CAG ACA AGC GTT ATT GAC CTC GGA TAT CCG Gly Ala Glu Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro 655 660 665	2010
GGC GTC CTG CCT GTT CTG AAC AAA GAA GCC GTT GAA TTC GCA ATG AAA Gly Val Leu Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys 670 675 680	2058
GCC GCT ATG GCG CTC AAC TGT GAG ATC GCA ACG GAT ACG AAG TTT GAC Ala Ala Met Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp 685 690 695	2106

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CGC AAA AAC TAT TTC TAT CCT GAC AAC CCG AAA GCG TAT CAG ATT TCT Arg Lys Asn Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser 700 705 710 715	2154
CAA TTT GAT AAG CCA ATC GGC GAA AAC GGC TGG ATC GAA ATT GAA GTC Gln Phe Asp Lys Thr Ile Gly Gln Asn Gly Trp Ile Glu Ile Glu Val 720 725 730	2202
GGC GGC AAA ACA AAA CGC ATC GGC ATC ACG CGC CTT CAT CTT GAA GAG Gly Gly Lys Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu 735 740 745	2250
GAT GCC GGA AAA CTG ACG CAT ACG GGC GAC GGC TAT TCT CTT GTT GAC Asp Ala Gly Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp 750 755 760	2298
TTC AAC CGT CAA GGA ACG CCG CTT GTT GAG TNC GTA TCA GAG CCG GAC Phe Asn Arg Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp 765 770 775	2346
ATC CGC ACG CCG GAA GAA NCG TAC GCA TAT CTT GAA AAG CTG AAA TCC Ile Arg Thr Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser 780 785 790 795	2394
ATC ATC CAA TAT ACA GGC GTT TCT GAC TGT AAA ATG GAA GAA GGC TCA Ile Ile Gln Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser 800 805 810	2442
CTT CGC TGT GAC GCC AAT ATC TCT CTT CGT CCG ATC GGC CAA GAG GAA Leu Arg Cys Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu 815 820 825	2490
TTC GGC ACA AAA ACA GAA TTG AAA AAC TTG AAC TCC TTT GCG TTT GTT Phe Gly Thr Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val 830 835 840	2538
CAA AAA GGC CTT GAG CAT GAA GAA AAA CCG CAG GAG CAG GTT CTT CTT Gln Lys Gly Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu 845 850 855	2586
TCC GGC TTC TTC ATC CAG CAA GAA ACT CCG CGT TAT GAT GAA GCA ACG Ser Gly Phe Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr 860 865 870 875	2634
AAG AAA ACC ATT CTT ATG CGT GTC AAA GAG GGA TCT GAC GAC TAC CGT Lys Lys Thr Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg 880 885 890	2682
TAC TTC CCA GAG CCA GAT CTA GTC GAG CTC TAC ATT GAT GAT GAA TGG Tyr Phe Pro Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp 895 900 905	2730
AAG GAA CGC GTA AAA GCA AGC ATT CCT GAG CTT CCG GAT GAG CGC CGC Lys Glu Arg Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg 910 915 920	2778
AAG CGT TAT ATC GAA GAG CTT GGC TTC GCT GCA TAT GAC GCA ATG GTT Lys Arg Tyr Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val 925 930 935	2826

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CTG ACG CTG ACA AAA GAA ATG GCT GAT TTC TTC GAA GAA ACC GTT CAA Leu Thr Leu Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln 940 945 950 955	2979
AAA GGC GCT GAA GCT AAA CAA GCG TCT AAC TGG CTG ATG GGT GAA GTG Lys Gly Ala Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val 960 965 970	2922
TCA GCT TAC CTA AAC GCA GAA CAA AAA GAG CTT GCC GAT GTT GCC CTG Ser Ala Tyr Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu 975 980 985	2970
ACA CCT GAA GGC CTT GCC GGC ATG ATC AAA TTG ATT GAA AAA GGA ACC Thr Pro Glu Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr 990 995 1000	3018
ATT TCT TCT AAG ATC GCG AAG AAA GTG TTT AAA GAA TTG ATT GAA AAA Ile Ser Ser Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys 1005 1010 1015	3066
GGC GGC GAC GCT GAG AAG ATT GTG AAA GAG AAA GGC CTT GTT CAG ATT Gly Gly Asp Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile 1020 1025 1030 1035	3114
TCT GAC GAA GGC GTG CTT CTG AAG CTT GTC ACT GAG GCG CTT GAC AAC Ser Asp Glu Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn 1040 1045 1050	3162
AAT CCT CAA TCA ATC GAA GAC TTT AAA AAC GGA AAA GAC CGC GCG ATC Asn Pro Gln Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile 1055 1060 1065	3210
GGC TTC CTA GTC GGA CAG ATT ATG AAA GCG TCC AAA GGA CAA GCC AAC Gly Phe Leu Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn 1070 1075 1080	3258
CCG CCG ATG GTC AAC AAA ATT CTG CTT GAA GAA ATT AAA AAA CGC Pro Pro Met Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg 1085 1090 1095	3303
TAATAA AAA AGC AGC CCT TAG AGG CTG CTT TTT TTA TGG TCA AAT Lys Ser Ser Pro Arg Leu Leu Phe Leu Trp Ser Asn 1100 1105 1110	3348
TGA GAT AAA GAC AAG ATG AGG GCC CGA AGC CTT TCA ACT TCT TTG TCG Asp Lys Asp Lys Met Arg Ala Arg Ser Leu Ser Thr Ser Leu Ser 1115 1120 1125	3396
TTG GTT CCG GCC AAA TTG GAC AGC ATG CCT TTA TAA TCG GCT TGC GCG Leu Val Pro Ala Lys Leu Asp Ser Met Pro Leu Ser Ala Cys Ala 1130 1135 1140	3444
GTT TAT CCT GAG TCA ATT CTT CCT CGA TAA GAT AAG TGA CAC GGT GAT Val Tyr Pro Glu Ser Ile Leu Pro Arg Asp Lys His Gly Asp 1145 1150	3492
ATC Ile 1155	3495

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2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(2) MOLECULE TYPE: protein

(3) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe
 1             5             10             15
Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val Asp
          20             25             30
His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu
          35             40             45
Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln
          50             55             60
Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr
          65             70             75             80
Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met
          85             90             95
Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys
          100            105            110
Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu
          115            120            125
Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu
          130            135            140
Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val
          145            150            155            160
Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala
          165            170            175
Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu
          180            185            190
Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met
          195            200            205
Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr
          210            215            220
Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr
          225            230            235            240
Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu
          245            250            255
Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr
          260            265            270

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Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser
 275 280 285
 Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser
 290 295 300
 Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys
 305 310 315 320
 Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly
 325 330 335
 Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg
 340 345 350
 Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp
 355 360 365
 Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser
 370 375 380
 Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu
 385 390 395 400
 Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala
 405 410 415
 Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser
 420 425 430
 Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser
 435 440 445
 Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly
 450 455 460
 Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr
 465 470 475 480
 Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly
 485 490 495
 Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala
 500 505 510
 Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu
 515 520 525
 Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys
 530 535 540
 Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile
 545 550 555 560
 Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met
 565 570 575
 Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His
 580 585 590

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Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gln
 595 600 605
 Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn
 610 615 620
 Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys
 625 630 635 640
 Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn
 645 650 655
 Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val
 660 665 670
 Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu
 675 680 685
 Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe
 690 695 700
 Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro
 705 710 715 720
 Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys
 725 730 735
 Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu
 740 745 750
 Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg Gln Gly
 755 760 765
 Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr Pro Glu
 770 775 780
 Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr
 785 790 795 800
 Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala
 805 810 815
 Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr
 820 825 830
 Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly Leu Glu
 835 840 845
 His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe Phe Ile
 850 855 860
 Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu
 865 870 875 880
 Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro
 885 890 895
 Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys
 900 905 910

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Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Glu
 915 920 925
 Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys
 930 935 940
 Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala
 945 950 955 960
 Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn
 965 970 975
 Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu
 980 985 990
 Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser Lys Ile
 995 1000 1005
 Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp Ala Glu
 1010 1015 1020
 Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu Gly Val
 1025 1030 1035 1040
 Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln Ser Ile
 1045 1050 1055
 Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu Val Gly
 1060 1065 1070
 Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met Val Asn
 1075 1080 1085
 Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg Lys Ser Ser Pro Arg Leu
 1090 1095 1100
 Leu Phe Leu Trp Ser Asn Asp Lys Asp Lys Met Arg Ala Arg Ser Leu
 1105 1110 1115 1120
 Ser Thr Ser Leu Ser Leu Val Pro Ala Lys Leu Asp Ser Met Pro Leu
 1125 1130 1135
 Ser Ala Cys Ala Val Tyr Pro Glu Ser Ile Leu Pro Arg Asp Lys His
 1140 1145 1150
 Gly Asp Ile
 1155

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

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BI LOCATION: 1..1458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA TTA TTT GAT CAT AAA ATC ACA GAA TTA AAA CAG CTC ATA CAT	48
Met Ser Leu Phe Asp His Lys Ile Thr Glu Leu Lys Gln Leu Ile His	
1 5 10 15	
AAA AAA GAG ATT AAG ATT TCT GAT CTG GTT GAT GAA TCT TAT AAA CGC	96
Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg	
20 25 30	
ATC CAA GCG GTT GAT GAT AAG GTA CAA GCC TTT TTG GCA TTA GAT GAA	144
Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu	
35 40 45	
GAA AGA GCG CGC GCA TAC GCG AAG GAG CTT GAT GAG GCG GTT GAC GGC	192
Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly	
50 55 60	
CGT TCT GAG CAC GGT CTT CTT TTC GGT ATG CCG ATC GGC GTA AAA GAT	240
Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp	
65 70 75 80	
AAT ATC GTA ACA AAA GGG CTG CGC ACA ACA TGC TCC AGC AAA ATT CTC	288
Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu	
85 90 95	
GAA AAC TTT GAT CCG ATT TAC GAT GCT ACT GTC GTT CAG CGC CTT CAA	336
Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln	
100 105 110	
GAC GCT GAA GCG GTC ACA ATC GGA AAA CTG AAC ATG GAC GAA TTC GCC	384
Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala	
115 120 125	
ATG GGG TCA TCT ACA GAA AAC TCA GCT TAC AAG CTG ACG AAA AAC CCT	432
Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro	
130 135 140	
TGG AAC CTG GAT ACA GTT CCC GGC GGT TCA AGC GGC GGA TCT GCA GCT	480
Trp Asn Leu Asp Thr Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala	
145 150 155 160	
GCG GTT GCT GCG GGA GAA GTT CCG TTT TCT CTT GGA TCT GAC ACA GGC	528
Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly	
165 170 175	
GGC TCC ATC CGT CAG CCG GCA TCT TTC TGC GGC GTT CTC GGA TTA AAA	576
Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys	
180 185 190	
CCT ACA TAC GGA CGT GTA TCT CGT TAC GGC CTG GTC GCA TTT GCG TCT	624
Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser	
195 200 205	
TCA TTG GAC CAA ATC GGA CCG ATT ACA CGT ACG GTT GAG GAT AAC GCG	672
Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala	
210 215 220	

TTT TTA CTT CAA GCG ATT TCC GGC GTA GAC AAA ATG GAC TCT ACG AGT 721
 Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser
 225 230 235 240

GCA AAT GTG GAC GTG CCT GAT TTT CTT TCT TCA TTA ACT GGC GAC ATC 769
 Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile
 245 250 255

AAA GGA CTG AAA ATC GCC GTT CCG AAA GAA TAC CTT GGT GAA GGT GTC 816
 Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val
 260 265 270

GGC AAA GAA GCG AGA GAA TCT GTC TTG GCA GCG CTG AAA GTC CTT GAA 864
 Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu
 275 280 285

GGT CTC GGC GCT ACA TGG GAA GAA GTG TCT CTT CCG CAC AGT AAA TAC 912
 Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr
 290 295 300

GCG CTT GCG ACA TAT TAC CTG CTG TCA TCT TCT GAA GCG TCA GCG AAC 960
 Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Glu Ala Ser Ala Asn
 305 310 315 320

CTT GCA CGC TTT GAC GGC ATC CGC TAC GGC TAC CGC ACA GAC AAC GCG 1008
 Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala
 325 330 335

GAT AAC CTG ATC GAC CTT TAC AAG CAA ACG CGC GCT GAA GGT TTC GGA 1056
 Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly
 340 345 350

AAT GAA GTC AAA CGC CGC ATC ATG CTC GGA ACG TTT GCT TTA AGC TCA 1104
 Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser
 355 360 365

GGC TAC TAC GAT GCG TAC TAC AAA AAA GCG CAA AAA GTG CGT ACG TTG 1152
 Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu
 370 375 380

ATT AAG AAG GAT TTC GAG GAC GTA TTT GAA AAA TAT GAT GTT ATT GTT 1200
 Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val
 385 390 395 400

GGA CCG ACT ACA CCG ACA CCT GCG TTT AAA ATC GGT GAA AAC ACG AAG 1248
 Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys
 405 410 415

GAT CCG CTC ACA ATG TAC GCA AAC GAT ATC TTA ACG ATT CCG GTC AAC 1296
 Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn
 420 425 430

CTT GCG GCG TAC CGG GAA TCA GGT GCC ATG CGG TTA GCA GAC GGA CTT 1344
 Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu
 435 440 445

CCG CTC GGC CTG CAA ATC ATC GGA AAA CAC TTT GAT GAA GCA CTG TAT 1392
 Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr
 450 455 460

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ACC GCG TTG CTC ATG CAT TTG AAC AAG CAA CAG ACC ATC ATA AAG CAA 1445
 Thr Ala Leu Leu Met His Leu Asn Lys Gln Gln Thr Ile Ile Lys Gln
 465 470 475 480

AAC CTG AAC TGT AAG GGG TGA 1461
 Asn Leu Asn Cys Lys Gly
 485

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Leu Phe Asp His Lys Ile Thr Glu Leu Lys Gln Leu Ile His
 1 5 10 15
 Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg
 20 25 30
 Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu
 35 40 45
 Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly
 50 55 60
 Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp
 65 70 75 80
 Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu
 85 90 95
 Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr Val Val Gln Arg Leu Gln
 100 105 110
 Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala
 115 120 125
 Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro
 130 135 140
 Trp Asn Leu Asp Thr Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala
 145 150 155 160
 Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly
 165 170 175
 Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys
 180 185 190
 Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser
 195 200 205
 Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala
 210 215 220

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Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser
 225 230 235 240
 Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile
 245 250 255
 Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val
 260 265 270
 Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu
 275 280 295
 Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr
 290 295 300
 Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Ser Glu Ala Ser Ala Asn
 305 310 315 320
 Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala
 325 330 335
 Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr Arg Ala Glu Gly Phe Gly
 340 345 350
 Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser
 355 360 365
 Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu
 370 375 380
 Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val
 385 390 395 400
 Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys
 405 410 415
 Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn
 420 425 430
 Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu
 435 440 445
 Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr
 450 455 460
 Thr Ala Leu Leu Met His Leu Asn Lys Gln Gln Thr Ile Ile Lys Gln
 465 470 475 480
 Asn Leu Asn Cys Lys Gly
 485

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

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1X) FEATURE:

A) NAME/KEY: CDS

B) LOCATION: 1..1485

1X1) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTG AAC TTT GAA ACG GTA ATC GGA CTT GAA GTC CAC GTT GAG TTA AAA Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys 1 5 10 15	43
ACA AAA TCA AAA ATT TTC TCA AGC TCT CCA ACG CCA TTC GGC GCG GAG Thr Lys Ser Lys Ile Phe Ser Ser Pro Thr Pro Phe Gly Ala Glu 20 25 30	96
GCG AAT ACG CAG ACA AGC GTT ATT GAC CTC GGA TAT CCG GGC GTC CTG Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu 35 40 45	144
CCT GTT CTG AAC AAA GAA GCC GTT GAA TTC GCA ATG AAA GCC GCT ATG Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met 50 55 60	192
GCG CTC AAC TGT GAG ATC GCA ACG GAT ACG AAG TTT GAC CGC AAA AAC Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn 65 70 75 80	240
TAT TTC TAT CCT GAC AAC CCG AAA GCG TAT CAG ATT TCT CAA TTT GAT Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp 85 90 95	288
AAG CCA ATC GGC GAA AAC GGC TGG ATC GAA ATT GAA GTC GGC GGC AAA Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys 100 105 110	336
ACA AAA CGC ATC GGC ATC ACG CGC CTT CAT CTT GAA GAG GAT GCC GGA Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly 115 120 125	384
AAA CTG ACG CAT ACG GGC GAC GGC TAT TCT CTT GTT GAC TTC AAC CGT Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg 130 135 140	432
CAA GGA ACG CCG CTT GTT GAG TNC GTA TCA GAG CCG GAC ATC CGC ACG Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr 145 150 155 160	480
CCG GAA GAA NCG TAC GCA TAT CTT GAA AAG CTG AAA TCC ATC ATC CAA Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln 165 170 175	528
TAT ACA GGC GTT TCT GAC TGT AAA ATG GAA GAA GGC TCA CTT CGC TGT Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys 180 185 190	576
GAC GCC AAT ATC TCT CTT CGT CCG ATC GGC CAA GAG GAA TTC GGC ACA Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr 195 200 205	624

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AAA ACA GAA TTG AAA AAC TTG AAC TCC TTT GCG TTT GTT CAA AAA GGC Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly 110 215 220	601
CTT GAG CAT GAA GAA AAA CGC CAG GAG CAG GTT CTT CTT TCC GGC TTC Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe 225 230 235 240	720
TTC ATC CAG CAA GAA ACT CGC CGT TAT GAT GAA GCA ACG AAG AAA ACC Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr 245 250 255	768
ATT CTT ATG CGT GTC AAA GAG GGA TCT GAC GAC TAC CGT TAC TTC CCA Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro 260 265 270	816
GAG CCA GAT CTA GTC GAG CTC TAC ATT GAT GAT GAA TGG AAG GAA CGC Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg 275 280 285	864
GTA AAA GCA AGC ATT CCT GAG CTT CCG GAT GAG CGC CGC AAG CGT TAT Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr 290 295 300	912
ATC GAA GAG CTT GGC TTC GCT GCA TAT GAC GCA ATG GTT CTG ACG CTG Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu 305 310 315 320	960
ACA AAA GAA ATG GCT GAT TTC TTC GAA GAA ACC GTT CAA AAA GGC GCT Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala 325 330 335	1008
GAA GCT AAA CAA GCG TCT AAC TGG CTG ATG GGT GAA GTG TCA GCT TAC Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr 340 345 350	1056
CTA AAC GCA GAA CAA AAA GAG CTT GCC GAT GTT GCC CTG ACA CCT GAA Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu 355 360 365	1104
GGC CTT GCC GGC ATG ATC AAA TTG ATT GAA AAA GGA ACC ATT TCT TCT Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser 370 375 380	1152
AAG ATC GCG AAG AAA GTG TTT AAA GAA TTG ATT GAA AAA GGC GGC GAC Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp 385 390 395 400	1200
GCT GAG AAG ATT GTG AAA GAG AAA GGC CTT GTT CAG ATT TCT GAC GAA Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu 405 410 415	1248
GGC GTG CTT CTG AAG CTT GTC ACT GAG GCG CTT GAC AAC AAT CCT CAA Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln 420 425 430	1296
TCA ATC GAA GAC TTT AAA AAC GGA AAA GAC CGC GCG ATC GGC TTC CTA Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu 435 440 445	1344

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GTC GGA CAG ATT ATG AAA GCG TCC AAA GGA CAA GCC AAC CCG CCG ATG 1390
 Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met
 450 455 460

GTC AAC AAA ATT CTG CTT GAA GAA ATT AAA AAA CGC TAA 1431
 Val Asn Lys Ile Leu Leu Gln Glu Ile Lys Lys Arg
 465 470 475

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys
 1 5 10 15
 Thr Lys Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu
 20 25 30
 Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu
 35 40 45
 Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met
 50 55 60
 Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn
 65 70 75 80
 Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp
 85 90 95
 Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys
 100 105 110
 Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly
 115 120 125
 Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg
 130 135 140
 Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr
 145 150 155 160
 Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln
 165 170 175
 Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys
 180 185 190
 Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr
 195 200 205
 Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly
 210 215 220

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Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe
225                      230                      235                      240
Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr
                      245                      250                      255
Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro
                      260                      265                      270
Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg
                      275                      280                      285
Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr
                      290                      295                      300
Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu
305                      310                      315                      320
Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala
                      325                      330                      335
Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr
                      340                      345                      350
Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu
                      355                      360                      365
Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser
                      370                      375                      380
Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp
385                      390                      395                      400
Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
                      405                      410                      415
Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln
                      420                      425                      430
Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu
                      435                      440                      445
Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met
                      450                      455                      460
Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
465                      470                      475

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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A: NAME/KEY: CDS
 B: LOCATION: 1..233

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TCA CGA ATT TCA ATA GAA GAA GTA AAG CAC GTT GCG CAC GTT GCA	48
Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala	
1 5 10 15	
AGA GTT GCG ATT ACT GAA GAA GAA GCA AAA ATG TTC ACT GAA CAG CTC	96
Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu	
20 25 30	
GAC AGT ATC ATT TCA TTT GCC GAG GAG CTT AAT GAG GTT AAC ACA GAC	144
Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp	
35 40 45	
AAT GTG GAG CCT ACA ACT CAC GTG CTG AAA ATG AAA AAT GTC ATG AGA	192
Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg	
50 55 60	
GAA GAT GAA GCG GGT AAA GGT CTT CCG GTT GAG GAT GTC ATG AAA AAT	240
Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn	
65 70 75 80	
GCG CCT GAC CAT AAA GAC GGC TAT ATT CGT GTG CCA TCA ATT CTG GAC	288
Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp	
85 90 95	
TAA	291

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala	15
1 5 10 15	
Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu	30
20 25 30	
Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp	45
35 40 45	
Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg	60
50 55 60	
Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn	75
65 70 75 80	
Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp	95
85 90 95	